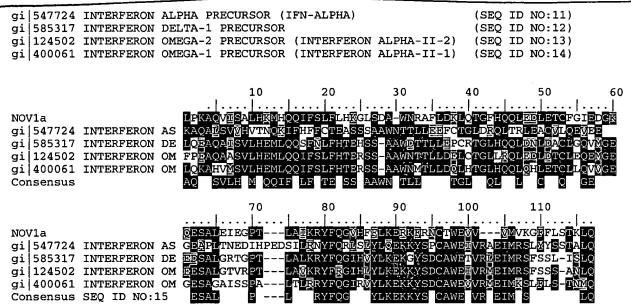
In the Specification:

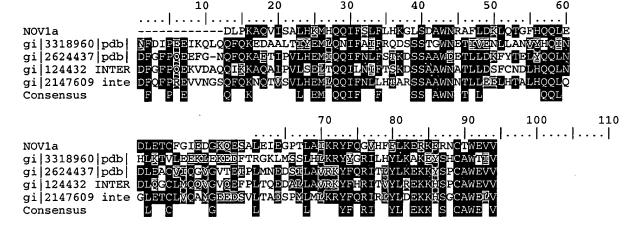


Replace the alignment starting on page 10, line 14 with the following alignment.



Replace the alignment starting on page 11, line 8 with the following alignment.

gi|3318960|pdb|1AU1|A Chain A, Human Interferon-Beta Crystal Structure (SEQ ID NO:16) gi|2624437|pdb|1RH2|A Chain A, Recombinant Human Interferon-Alpha 2b (SEQ ID NO:17) gi|124432 INTERFERON ALPHA-1 PRECURSOR (SEQ ID NO:18) gi|2147609 interferon-omega20 - rabbit (SEQ ID NO:19) Consensus (SEQ ID NO:20)





This same alignment between KIAA1246 (SEQ ID NO:27) and NOV2 (identified as

AF038458A) is shown below.

Replace the alignment starting on page 21, line 1 with the following alignment.

KIAA_predicted	METLLGGLLAF@MAFAVVDACPKYCVCQNLSESLGTLCPSKGLLFVPPDØDRR
AF038458_A	MANLPLLCLLPLAPASSPPQSATPSPCPRRCRCQTQSLPLSVLCPGAGLLFVPPSLDRR
KIAA_predicted	TVELRLEGNFIIH IS ROD FANMTGL WOLDES RNTISH I OPFS FLOLES LRS LHLDS NRLP
RICK_AF038458_A	AAELRLADNFIAS WRRRD LANMTGLEHLS LS RNTIRHWAAGAFADLRALRALHLDGNELT
KIAA_predicted	SLGEDTLRGLVNL <mark>QHLIVN</mark> NNQLGGADEAFEDFLLTLEDLDLSYNNLHGLPWDSVRRMV
AF038458_A	SLGEGQLRGLVNLRHLILSNNQLAALAGALDDCAETLEDLDLSYNNLEQLPWEALGRLG
KIAA_predicted	NÜHQLSLDHNLLDH NA EGT FADL QKLAR LDÜTSNRLQKÜP. EDP NFARSQASAL TATP FAP
AF038458_A	NYNTLGLDHNLLAS WPAGAFSRLHKLAR LDMTSNRETT NP EDP NESELPL LAR PRGSPAS
KIAA_predicted	PLSFSFGGNPLHCNCELLWLRRLERDDDLETCGSPGGLKGRYFWHVREEEFVCEPPLUTQ
AF038458_A	ALVLAFGGNPLHCNCELWWLRRLARDDDLEACASPPALGGRYFWAVGEEEFVCEPPWVTH
KIAA_predicted	HIJHKLLVLEGQAAT LIKCKANGOP SPLUHWVAPDDRLVGNSSRTAVYDNGTLDUFUTTSQD
AF038458_A	RSPPLAW. AGRPAALRCRAVGOP EPRVRWVSPQGRLUGNSSRARAFPNGTLELLVTEPGD
KIAA_predicted	SGAFTCIAANAAGEATAMVEVSIVQLPHLSNSTSRTAPPKSRLSDITGSSKTSRGGGG
AF038458_A	GGIFTCIAANAAGEATAAVELTVGPPPPPQLANSTSCDPPRDGDPDALTPPSAASAS
KIAA_predicted	SGGGEPPKSPPERAVLVSEVTTTSALVKWSVSKSAPRVKMYQLQYNCSDDEVLLYYRMIPA
AF038458_A	AKVADTG-PPTDRGVQVTEHGATAALVQWPDQRPIPGKRMYQLQYNSSADDLLVYRMIPA
KIAA_predicted	SNKAFVVNNLVSGT GVDLCVLAMWDDNATTLTATNIVGCAQFFTKADYPQCQSMHSQILG
AF038458_A	ESRSFLLTDLASGRTVDLCVLAWYBDSATGLTATRPVGCARFSTEPALRPCGAPHAPFLG
KIAA_predicted	GTMILVNGGNIVARLLVFIVNLMVRYKVCNHEAPSKMAAAVSNVYSQTNGAQPPPPPSS
AF038458_A	GTMINALGGVIVASVLVFIFNLLMRYKVHGGQPPGKAKNPAPVŠSVCSQTNGALGPTPN-
KIAA_predicted AF038458_A	APAGAPPQGPPKVVVRNELLDFTASLARASDSSSSSSLGSGEAAGLGRAPWRIPPSAPRFPAPPAPEP
KIAA_predicted AF038458_A	KPSLDRLMGAFAS LD LKS QRKEE LLDSRT PAGRGAGTSARGHH SDREPLLGP PAARARS L
KIAA_predicted AF038458_A	L PLPLEGKAKRSHS F DMG D FAA A AAGGV V P GGYSPPRKV SN I WT KRSLS V N GM LLP F EE S
KIAA_predicted AF038458_A	DLVGARGTFGSSEWVMESTV

